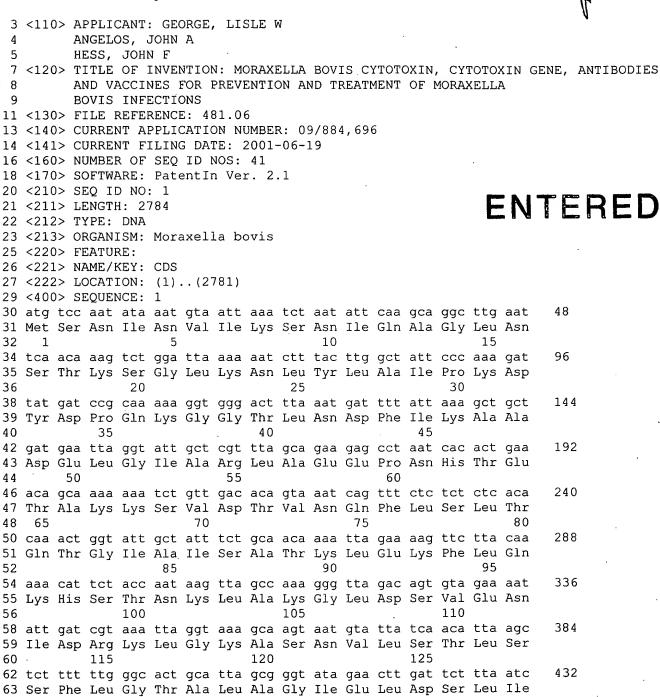0590
0905

OIPE

#3

RAW SEQUENCE LISTING   DATE: 09/06/2001
PATENT APPLICATION: US/09/884,696   TIME: 15:20:38
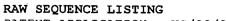
Input Set : A:\481-06.app
Output Set: N:\CRF3\09062001\I884696.raw

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 3 <110> APPLICANT: GEORGE, LISLE W
 4         ANGELOS, JOHN A
 5         HESS, JOHN F
 7 <120> TITLE OF INVENTION: MORAXELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES
 8         AND VACCINES FOR PREVENTION AND TREATMENT OF MORAXELLA
 9         BOVIS INFECTIONS
11 <130> FILE REFERENCE: 481.06
13 <140> CURRENT APPLICATION NUMBER: 09/884,696
14 <141> CURRENT FILING DATE: 2001-06-19
16 <160> NUMBER OF SEQ ID NOS: 41
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2784
22 <212> TYPE: DNA
23 <213> ORGANISM: Moraxella bovis
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(2781)
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32  1               5                  10                  15
34 tca aca aag tct gga tta aaa aat ctt tac ttg gct att ccc aaa gat    96
35 Ser Thr Lys Ser Gly Leu Lys Asn Leu Tyr Leu Ala Ile Pro Lys Asp
36             20                  25                  30
38 tat gat ccg caa aaa ggt ggg act tta aat gat ttt att aaa gct gct   144
39 Tyr Asp Pro Gln Lys Gly Gly Thr Leu Asn Asp Phe Ile Lys Ala Ala
40          35                  40                  45
42 gat gaa tta ggt att gct cgt tta gca gaa gag cct aat cac act gaa   192
43 Asp Glu Leu Gly Ile Ala Arg Leu Ala Glu Glu Pro Asn His Thr Glu
44       50                  55                  60
46 aca gca aaa aaa tct gtt gac aca gta aat cag ttt ctc tct ctc aca   240
47 Thr Ala Lys Lys Ser Val Asp Thr Val Asn Gln Phe Leu Ser Leu Thr
48 65                  70                  75                  80
50 caa act ggt att gct att tct gca aca aaa tta gaa aag ttc tta caa   288
51 Gln Thr Gly Ile Ala Ile Ser Ala Thr Lys Leu Glu Lys Phe Leu Gln
52                 85                  90                  95
54 aaa cat tct acc aat aag tta gcc aaa ggg tta gac agt gta gaa aat   336
55 Lys His Ser Thr Asn Lys Leu Ala Lys Gly Leu Asp Ser Val Glu Asn
56             100                 105                 110
58 att gat cgt aaa tta ggt aaa gca agt aat gta tta tca aca tta agc   384
59 Ile Asp Arg Lys Leu Gly Lys Ala Ser Asn Val Leu Ser Thr Leu Ser
60             115                 120                 125
62 tct ttt ttg ggc act gca tta gcg ggt ata gaa ctt gat tct tta atc   432
63 Ser Phe Leu Gly Thr Ala Leu Ala Gly Ile Glu Leu Asp Ser Leu Ile
64          130                 135                 140
66 aaa aaa ggt gat gct gca cct gat gct ttg gct aaa gct agt att gac   480
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67 Lys Lys Gly Asp Ala Ala Pro Asp Ala Leu Ala Lys Ala Ser Ile Asp
68 145               150               155               160
70 ttg att aat gag ata att ggt aat cta tct cag agt act caa acg att     528
71 Leu Ile Asn Glu Ile Ile Gly Asn Leu Ser Gln Ser Thr Gln Thr Ile
72               165               170               175
74 gaa gca ttt tct tca cag tta gca aag tta ggt tct act ata tcg cag     576
75 Glu Ala Phe Ser Ser Gln Leu Ala Lys Leu Gly Ser Thr Ile Ser Gln
76               180               185               190
78 gct aaa ggc ttc tct aat ata gga aac aag ttg caa aac tta aat ttt     624
79 Ala Lys Gly Phe Ser Asn Ile Gly Asn Lys Leu Gln Asn Leu Asn Phe
80           195               200               205
82 tct aaa aca aat ctt ggt ttg gaa ata att act ggt ttg cta tca ggc     672
83 Ser Lys Thr Asn Leu Gly Leu Glu Ile Ile Thr Gly Leu Leu Ser Gly
84       210               215               220
86 att tct gca ggc ttt gct tta gcg gat aaa aat gca tcg act ggc aaa     720
87 Ile Ser Ala Gly Phe Ala Leu Ala Asp Lys Asn Ala Ser Thr Gly Lys
88 225               230               235               240
90 aaa gtt gct gca ggt ttt gaa tta agc aat caa gtt att ggt aat gta     768
91 Lys Val Ala Ala Gly Phe Glu Leu Ser Asn Gln Val Ile Gly Asn Val
92               245               250               255
94 aca aaa gca att tct tca tat gtt tta gca caa cgt gtt gct gct ggt     816
95 Thr Lys Ala Ile Ser Ser Tyr Val Leu Ala Gln Arg Val Ala Ala Gly
96           260               265               270
98 cta tca act act ggt gct gtt gct gct tta att act tca tcg att atg     864
99 Leu Ser Thr Thr Gly Ala Val Ala Ala Leu Ile Thr Ser Ser Ile Met
100           275               280               285
102 ttg gca att agt cct ttg gca ttt atg aat gca gca gat aaa ttc aat    912
103 Leu Ala Ile Ser Pro Leu Ala Phe Met Asn Ala Ala Asp Lys Phe Asn
104       290               295               300
106 cat gct aat gct ctt gat gag ttt gca aaa caa ttc cga aaa ttt ggc    960
107 His Ala Asn Ala Leu Asp Glu Phe Ala Lys Gln Phe Arg Lys Phe Gly
108 305               310               315               320
110 tat gat ggg gat cat tta ttg gct gaa tat cag cgt ggt gtg ggt act    1008
111 Tyr Asp Gly Asp His Leu Leu Ala Glu Tyr Gln Arg Gly Val Gly Thr
112               325               330               335
114 att gaa gct tca tta act aca att agt acg gca tta ggt gca gtt tct    1056
115 Ile Glu Ala Ser Leu Thr Thr Ile Ser Thr Ala Leu Gly Ala Val Ser
116           340               345               350
118 gct ggt gtt tcc gct gct gct gta gga tct gct gtt ggt gca ccg att    1104
119 Ala Gly Val Ser Ala Ala Ala Val Gly Ser Ala Val Gly Ala Pro Ile
120           355               360               365
122 gca cta tta gtt gca ggt gtt aca gga ttg atc tct gga att tta gaa    1152
123 Ala Leu Leu Val Ala Gly Val Thr Gly Leu Ile Ser Gly Ile Leu Glu
124       370               375               380
126 gcg tct aaa cag gca atg ttt gaa agt gtt gct aac cgt tta caa ggt    1200
127 Ala Ser Lys Gln Ala Met Phe Glu Ser Val Ala Asn Arg Leu Gln Gly
128 385               390               395               400
130 aaa att tta gag tgg gaa aag caa aat ggc ggt cag aac tat ttt gat    1248
131 Lys Ile Leu Glu Trp Glu Lys Gln Asn Gly Gly Gln Asn Tyr Phe Asp
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132                   405                410                415
134 aaa ggc tat gat tct cgt tat gct gct tat tta gct aat aac tta aaa   1296
135 Lys Gly Tyr Asp Ser Arg Tyr Ala Ala Tyr Leu Ala Asn Asn Leu Lys
136                   420            .    425                430
138 ttt ttg tct gag cta aat aaa gag ttg gaa gct gaa cgt gtt att gca   1344
139 Phe Leu Ser Glu Leu Asn Lys Glu Leu Glu Ala Glu Arg Val Ile Ala
140             435                440                445
142 atc acc caa caa cgt tgg gat aat aat att ggt gag tta gca ggt att   1392
143 Ile Thr Gln Gln Arg Trp Asp Asn Asn Ile Gly Glu Leu Ala Gly Ile
144  ·  450                455                460
146 acc aaa ttg ggt gaa cgc att aag agc gga aaa gct tat gca gat gct   1440
147 Thr Lys Leu Gly Glu Arg Ile Lys Ser Gly Lys Ala Tyr Ala Asp Ala
148 465                   470                475                480
150 ttt gaa gat ggc aag aaa gtt gaa gct ggt tcc aat att act ttg gat   1488
151 Phe Glu Asp Gly Lys Lys Val Glu Ala Gly Ser Asn Ile Thr Leu Asp
152                   485                490                495
154 gct aaa act ggt atc ata gac att agt aat tca aat ggg aaa aaa acg   1536
155 Ala Lys Thr Gly Ile Ile Asp Ile Ser Asn Ser Asn Gly Lys Lys Thr
156             500                505                510
158 caa gcg ttg cat ttc act tcg cct ttg tta aca gca gga act gaa tca   1584
159 Gln Ala Leu His Phe Thr Ser Pro Leu Leu Thr Ala Gly Thr Glu Ser
160             515                520                525
162 cgt gaa cgt tta act aat ggt aaa tac tct tat att aat aag tta aaa   1632
163 Arg Glu Arg Leu Thr Asn Gly Lys Tyr Ser Tyr Ile Asn Lys Leu Lys
164       530                535                540
166 ttc gga cgt gta aaa aac tgg caa gtt aca gat gga gag gct agt tct   1680
167 Phe Gly Arg Val Lys Asn Trp Gln Val Thr Asp Gly Glu Ala Ser Ser
168 545                   550                555                560
170 aaa tta gat ttc tct aaa gtt att cag cgt gta gcc gag aca gaa ggc   1728
171 Lys Leu Asp Phe Ser Lys Val Ile Gln Arg Val Ala Glu Thr Glu Gly
172             565                570                575
174 aca gac gag att ggt cta ata gta aat gca aaa gct ggc aat gac gat   1776
175 Thr Asp Glu Ile Gly Leu Ile Val Asn Ala Lys Ala Gly Asn Asp Asp
176             580                585                590
178 atc ttt gtt ggt caa ggt aaa atg aat att gat ggt gga gat gga cac   1824
179 Ile Phe Val Gly Gln Gly Lys Met Asn Ile Asp Gly Gly Asp Gly His
180             595                600      .         605
182 gat cgt gtc ttc tat agt aaa gac gga gga ttt ggt aat att act gta   1872
183 Asp Arg Val Phe Tyr Ser Lys Asp Gly Gly Phe Gly Asn Ile Thr Val
184       610                615     .         620
186 gat ggt acg agt gca aca gaa gca ggc agt tat aca gtt aat cgt aag   1920
187 Asp Gly Thr Ser Ala Thr Glu Ala Gly Ser Tyr Thr Val Asn Arg Lys
188 625                   630             .    635                640
190 gtt gct cga ggt gat atc tac cat gaa gtt gtg aag cgt caa gaa acc   1968
191 Val Ala Arg Gly Asp Ile Tyr His Glu Val Val Lys Arg Gln Glu Thr
192             645                650 ·              655
194 aag gtg ggt aaa cgt act gaa act atc cag tat cgt gat tat gaa tta   2016
195 Lys Val Gly Lys Arg Thr Glu Thr Ile Gln Tyr Arg Asp Tyr Glu Leu
196       ·  660                665                670
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198 aga aaa gtt ggg tat ggt tat cag tct acc gat aat ttg aaa tca gta   2064
199 Arg Lys Val Gly Tyr Gly Tyr Gln Ser Thr Asp Asn Leu Lys Ser Val
200         675                 680                 685
202 gaa gaa gta att ggt tct caa ttt aat gat gta ttc aaa ggt tct aaa   2112
203 Glu Glu Val Ile Gly Ser Gln Phe Asn Asp Val Phe Lys Gly Ser Lys
204         690                 695                 700
206 ttc aac gac ata ttc cat agt ggt gaa ggt gat gat tta ctc gat ggt   2160
207 Phe Asn Asp Ile Phe His Ser Gly Glu Gly Asp Asp Leu Leu Asp Gly
208 705                 710                 715                 720
210 ggt gct ggt gac gac cgc ttg ttt ggt ggt aaa ggc aac gat cga ctt   2208
211 Gly Ala Gly Asp Asp Arg Leu Phe Gly Gly Lys Gly Asn Asp Arg Leu
212                 725                 730                 735
214 tct gga gat gaa ggc gat gat tta ctc gat ggc ggt tct ggt gat gat   2256
215 Ser Gly Asp Glu Gly Asp Asp Leu Leu Asp Gly Gly Ser Gly Asp Asp
216         740                 745                 750
218 gta tta aat ggt ggt gct ggt aat gat gtc tat atc ttt cgg aaa ggt   2304
219 Val Leu Asn Gly Gly Ala Gly Asn Asp Val Tyr Ile Phe Arg Lys Gly
220         755                 760                 765
222 gat ggt aat gat act ttg tac gat ggc acg ggc aat gat aaa tta gca   2352
223 Asp Gly Asn Asp Thr Leu Tyr Asp Gly Thr Gly Asn Asp Lys Leu Ala
224         770                 775                 780
226 ttt gca gat gca aat ata tct gat att atg att gaa cgt acc aaa gag   2400
227 Phe Ala Asp Ala Asn Ile Ser Asp Ile Met Ile Glu Arg Thr Lys Glu
228 785                 790                 795                 800
230 ggt att ata gtt aaa cga aat gat cat tca ggt agt att aac ata cca   2448
231 Gly Ile Ile Val Lys Arg Asn Asp His Ser Gly Ser Ile Asn Ile Pro
232                 805                 810                 815
234 aga tgg tac ata aca tca aat tta caa aat tat caa agt aat aaa aca   2496
235 Arg Trp Tyr Ile Thr Ser Asn Leu Gln Asn Tyr Gln Ser Asn Lys Thr
236                 820                 825                 830
238 gat cat aaa att gag caa cta att ggt aaa gat ggt agt tat atc act   2544
239 Asp His Lys Ile Glu Gln Leu Ile Gly Lys Asp Gly Ser Tyr Ile Thr
240         835                 840                 845
242 tcc gat caa att gat aaa att ttg caa gat aag aaa gat ggt aca gta   2592
243 Ser Asp Gln Ile Asp Lys Ile Leu Gln Asp Lys Lys Asp Gly Thr Val
244         850                 855                 860
246 att aca tct caa gaa ttg aaa aag ctt gct gat gag aat aag agc caa   2640
247 Ile Thr Ser Gln Glu Leu Lys Lys Leu Ala Asp Glu Asn Lys Ser Gln
248 865                 870                 875                 880
250 aaa tta tct gct tcg gac att gca agt agc tta aat aag cta gtt ggg   2688
251 Lys Leu Ser Ala Ser Asp Ile Ala Ser Ser Leu Asn Lys Leu Val Gly
252                 885                 890                 895
254 tca atg gca cta ttt ggt aca gca aat agt gtg agt tct aac gcc tta   2736
255 Ser Met Ala Leu Phe Gly Thr Ala Asn Ser Val Ser Ser Asn Ala Leu
256                 900                 905                 910
258 cag cca att aca caa cca act caa gga att ttg gct cca agt gtt tag   2784
259 Gln Pro Ile Thr Gln Pro Thr Gln Gly Ile Leu Ala Pro Ser Val
260         915                 920                 925
263 <210> SEQ ID NO: 2
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RAW SEQUENCE LISTING   DATE: 09/06/2001
PATENT APPLICATION: US/09/884,696   TIME: 15:20:38

Input Set : A:\481-06.app
Output Set: N:\CRF3\09062001\I884696.raw

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265 <212> TYPE: PRT
266 <213> ORGANISM: Moraxella bovis
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273             20                  25                  30
275 Tyr Asp Pro Gln Lys Gly Gly Thr Leu Asn Asp Phe Ile Lys Ala Ala
276         35                  40                  45
278 Asp Glu Leu Gly Ile Ala Arg Leu Ala Glu Glu Pro Asn His Thr Glu
279     50                  55                  60
281 Thr Ala Lys Lys Ser Val Asp Thr Val Asn Gln Phe Leu Ser Leu Thr
282 65                  70                  75                  80
284 Gln Thr Gly Ile Ala Ile Ser Ala Thr Lys Leu Glu Lys Phe Leu Gln
285             85                  90                  95
287 Lys His Ser Thr Asn Lys Leu Ala Lys Gly Leu Asp Ser Val Glu Asn
288             100                 105                 110
290 Ile Asp Arg Lys Leu Gly Lys Ala Ser Asn Val Leu Ser Thr Leu Ser
291         115                 120                 125
293 Ser Phe Leu Gly Thr Ala Leu Ala Gly Ile Glu Leu Asp Ser Leu Ile
294         130                 135                 140
296 Lys Lys Gly Asp Ala Ala Pro Asp Ala Leu Ala Lys Ala Ser Ile Asp
297 145                 150                 155                 160
299 Leu Ile Asn Glu Ile Ile Gly Asn Leu Ser Gln Ser Thr Gln Thr Ile
300             165                 170                 175
302 Glu Ala Phe Ser Ser Gln Leu Ala Lys Leu Gly Ser Thr Ile Ser Gln
303             180                 185                 190
305 Ala Lys Gly Phe Ser Asn Ile Gly Asn Lys Leu Gln Asn Leu Asn Phe
306         195                 200                 205
308 Ser Lys Thr Asn Leu Gly Leu Glu Ile Ile Thr Gly Leu Leu Ser Gly
309     210                 215                 220
311 Ile Ser Ala Gly Phe Ala Leu Ala Asp Lys Asn Ala Ser Thr Gly Lys
312 225                 230                 235                 240
314 Lys Val Ala Ala Gly Phe Glu Leu Ser Asn Gln Val Ile Gly Asn Val
315             245                 250                 255
317 Thr Lys Ala Ile Ser Ser Tyr Val Leu Ala Gln Arg Val Ala Ala Gly
318         260                 265                 270
320 Leu Ser Thr Thr Gly Ala Val Ala Ala Leu Ile Thr Ser Ser Ile Met
321         275                 280                 285
323 Leu Ala Ile Ser Pro Leu Ala Phe Met Asn Ala Ala Asp Lys Phe Asn
324     290                 295                 300
326 His Ala Asn Ala Leu Asp Glu Phe Ala Lys Gln Phe Arg Lys Phe Gly
327 305                 310                 315                 320
329 Tyr Asp Gly Asp His Leu Leu Ala Glu Tyr Gln Arg Gly Val Gly Thr
330             325                 330                 335
332 Ile Glu Ala Ser Leu Thr Thr Ile Ser Thr Ala Leu Gly Ala Val Ser
333             340                 345                 350
335 Ala Gly Val Ser Ala Ala Ala Val Gly Ser Ala Val Gly Ala Pro Ile
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—) Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 09/06/2001
PATENT APPLICATION: US/09/884,696   TIME: 15:20:39

Input Set : A:\481-06.app
Output Set: N:\CRF3\09062001\I884696.raw

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L:1157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:2825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
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